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DEC 18 2001

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/848,915A

DATE: 11/26/2001

TIME: 12:17:13

Input Set : N:\Crif3\RULE60\09848915A.txt

Output Set: N:\CRF3\11262001\I848915A.raw

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: Hillman, Jennifer L.

8 Goli, Surya K.

C--> 10 (ii) TITLE OF INVENTION: NOVEL TUMORIGENESIS PROTEIN

12 (iii) NUMBER OF SEQUENCES: 3

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

16 (B) STREET: 3174 Porter Drive

17 (C) CITY: Palo Alto

18 (D) STATE: CA

19 (E) COUNTRY: USA

20 (F) ZIP: 94304

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Diskette

24 (B) COMPUTER: IBM Compatible

25 (C) OPERATING SYSTEM: DOS

26 (D) SOFTWARE: FastSEQ for Windows Version 2.0

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/848,915A

C--> 30 (B) FILING DATE: 04-May-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/183,825

35 (B) FILING DATE: 1998-10-30

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Billings, Lucy J.

40 (B) REGISTRATION NUMBER: 36,749

41 (C) REFERENCE/DOCKET NUMBER: PF-0247 US

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 415-855-0555

45 (B) TELEFAX: 415-845-4166

46 (C) TELEX:

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 195 amino acids

53 (B) TYPE: amino acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (vii) IMMEDIATE SOURCE:

58 (A) LIBRARY: UTRSNOT02

59 (B) CLONE: 2267574

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

63 Met Glu Leu Ser Glu Ser Val Gln Lys Gly Phe Gln Met Leu Ala Asp

64 1 5 10 15

65 Pro Arg Ser Phe Asp Ser Asn Ala Phe Thr Leu Leu Leu Arg Ala Ala

66 20 25 30

ENTERED

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67 Phe Gln Ser Leu Leu Asp Ala Gln Ala Asp Glu Ala Val Leu Asp His
68      35      40      45
69 Pro Asp Leu Lys His Ile Asp Pro Val Val Leu Lys His Cys His Ala
70      50      55      60
71 Ala Ala Ala Thr Tyr Ile Leu Glu Ala Gly Lys His Arg Ala Asp Lys
72      65      70      75      80
73 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg
74      85      90      95
75 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu
76      100     105     110
77 Ile Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val
78      115     120     125
79 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Arg Met
80      130     135     140
81 Tyr Arg Pro Ala Tyr Leu Val Thr Leu Ser Val Gln Asn Thr Asp Ser
82      145     150     155     160
83 Pro Ser Tyr Pro Glu Ile Ser Phe Ser Cys Ser Met Glu Gln Leu Gln
84      165     170     175
85 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala
86      180     185     190
87 Thr Gln Leu
88      195

```

90 (2) INFORMATION FOR SEQ ID NO: 2:

92 (i) SEQUENCE CHARACTERISTICS:

93 (A) LENGTH: 751 base pairs

94 (B) TYPE: nucleic acid

95 (C) STRANDEDNESS: single

96 (D) TOPOLOGY: linear

98 (vii) IMMEDIATE SOURCE:

99 (A) LIBRARY: UTRSN02

100 (B) CLONE: 2267574

102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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104 CGAAGTCACG GCGCGCTCAC AATGGAGCTC TCGGAGTCTG TGCAGAAAGG CTTCCAGATG      60
105 CTGGCGGATC CCCGCTCCTT CGACTCCAAC GCCTTCACGC TTCTCCTCCG GGCGGCATTC      120
106 CAGAGTCTGC TGGACGCCCA GGCGGACGAG GCCGTGTTAG ATCATCCAGA CTTGAAACAT      180
107 ATCGACCCAG TGGTTTTTAA ACATTGTCAT GCAGCAGCTG CAACTTACAT ACTAGAGGCA      240
108 GGAAAGCACC GAGCTGACAA GTCAACTCTA AGCACTTATC TAGAAGACTG TAAATTGAC      300
109 AGAGAGCGAA TAGAACTGTT TTGCACGGAA TATCAGAATA ATAAGAATTC CCTAGAAATC      360
110 CTACTGGGAA GTATAGGCAG ATCTCTCCCT CATATAACGG ATGTTTCTTG GCGCTTGGA      420
111 TATCAGATAA AGACCAATCA ACTTCATAGG ATGTACAGAC CTGCATATTT GGTGACCTTA      480
112 AGTGTAACAG ACACTGATTC CCCATCCTAT CCAGAGATTA GTTTTAGTTG CAGCATGGAA      540
113 CAATTACAGG ACTTGGTGGG GAAACTTAAA GATGCTTCGA AAAGCCTGGA AAGAGCAACT      600
114 CAGTTGTAAC TTGGGGAAGT TAACGATCCG CCCGAGTGCA GAGGAAAACC AGAAACGCCT      660
115 TGCCTTCAGC TGAACCACCG TTTGTGCGAG CTGGATGTCC TTTTCAGTAG AAAAGAATTT      720
116 TCCTTTTGAA TTTATACCAT TCANCAATTT T
117                                     751

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118 (2) INFORMATION FOR SEQ ID NO: 3:

120 (i) SEQUENCE CHARACTERISTICS:

121 (A) LENGTH: 195 amino acids

122 (B) TYPE: amino acid

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123      (C) STRANDEDNESS: single
124      (D) TOPOLOGY: linear
126      (vii) IMMEDIATE SOURCE:
127          (A) LIBRARY: GenBank
128          (B) CLONE: 265569
130      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
132 Met Glu Leu Ser Glu Ser Val Gln Arg Gly Ile Gln Thr Leu Ala Asp
133 1      5      10      15
134 Pro Gly Ser Phe Asp Ser Asn Ala Phe Ala Leu Leu Leu Arg Ala Ala
135      20      25      30
136 Phe Gln Ser Leu Leu Asp Ala Arg Ala Asp Glu Ala Ala Leu Asp His
137      35      40      45
138 Pro Tyr Leu Lys Gln Ile Asp Pro Val Val Leu Lys His Cys His Ala
139      50      55      60
140 Ala Ala Ala Thr Cys Ile Leu Glu Ala Gly Lys His Gln Val Asp Lys
141 65      70      75      80
142 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg
143      85      90      95
144 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu
145      100     105     110
146 Thr Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val
147      115     120     125
148 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Lys Met
149      130     135     140
150 Tyr Arg Pro Gly Tyr Leu Val Thr Leu Asn Val Glu Asn Asn Asp Ser
151 145     150     155     160
152 Gln Ser Tyr Pro Glu Ile Asn Phe Ser Cys Asn Met Glu Gln Leu Gln
153      165     170     175
154 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala
155      180     185     190
156 Thr Gln Leu
157      195

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VERIFICATION SUMMARY

DATE: 11/26/2001

PATENT APPLICATION: US/09/848,915A

TIME: 12:17:14

Input Set : N:\Crf3\RULE60\09848915A.txt

Output Set: N:\CRF3\11262001\I848915A.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]